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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/965,825DATE: 11/07/2001
TIME: 14:41:53Input Set : A:\es.txt
Output Set: N:\CRF3\11072001\I965825.raw

3 <110> APPLICANT: DUSCH, Nicole
 4 THOMAS, Hermann
 5 THIERBACH, Georg
 7 <120> TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHEINOIC ACID USING
 8 CORYNEFORM BACTERIA
 10 <130> FILE REFERENCE: 21354US0X
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/965,825 O/P
 C--> 12 <141> CURRENT FILING DATE: 2001-10-01
 12 <150> PRIOR APPLICATION NUMBER: DE 10048604.5
 13 <151> PRIOR FILING DATE: 2000-09-30
 15 <150> PRIOR APPLICATION NUMBER: DE 10117085.8
 16 <151> PRIOR FILING DATE: 2001-04-06
 18 <160> NUMBER OF SEQ ID NOS: 14
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 2160
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Corynebacterium glutamicum
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (327)..(2063)
 30 <223> OTHER INFORMATION:
 33 <220> FEATURE:
 34 <221> NAME/KEY: -35_signal
 35 <222> LOCATION: (227)..(232)
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 39 <220> FEATURE:
 40 <221> NAME/KEY: -10_signal
 41 <222> LOCATION: (256)..(261)
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 46 tttagaggcga ttctgtgagg tcaacttttg tgggttcggg gtctaaattt gcccagtttt 60
 48 cgaggcacc agacaggcgt gcccacatgg tttaaatagg cgatctgtgg gcacatctgt 120
 50 ttgggttcga cgggctgaaa ccaaaccaga tgcccaacggc acacggaaaa tccaaaaagt 180
 52 ggccatccct gttttgtacc gagttacccac cggggctgaa aactccctgg caggcggcgc 240
 54 aacgcgtggca acaactggaa tttaagagaca caatttgaatg cgcacccaatg taggcaacac 300
 56 aataggccata acgttgaggaa gttcag atg gca cac agc tac gca gaa caa tta 353
 57 Met Ala His Ser Tyr Ala Glu Gln Leu
 58 1 5
 60 att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg 401
 61 Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val
 62 10 15 20 25
 64 ggt gac agc ctt aat ccc atc gtg gat gtc gtc cgc caa tca gat att 449
 65 Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile
 66 30 35 40
 68 gag tgg gtg cac gtt cga aat gag gaa gca ggc gcg ttt gca gcc ggt 497
 69 Glu Trp Val His Val Arg Asn Glu Ala Ala Ala Phe Ala Ala Gly

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70	45	50	55		
72	gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt			545	
73	Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys				
74	60	65	70		
76	ggt cct gga aac aca cac ctg att cag ggt ctt tat gat tcg cat cga			593	
77	Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr Asp Ser His Arg				
78	75	80	85		
80	aat ggt ggc aag gtc ttg gcc atc gct agc cat att ccg agt gcc gag			641	
81	Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile Pro Ser Ala Gln				
82	90	95	100	105	
84	att ggt tcg acg ttc cag aac acg cat ccg gag att ttg ttt aag			689	
85	Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu Ile Leu Phe Lys				
86	110	115	120		
88	gaa tgc tct ggt tac tgc gag atg gtc aat ggt ggt gag cag ggt gaa			737	
89	Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly Glu Gln Gly Glu				
90	125	130	135		
92	cgc att ttg cat cac gcg att cag tcc acc atg gcg ggt aaa ggt gtg			785	
93	Arg Ile Leu His Ala Ile Gln Ser Thr Met Ala Gly Lys Gly Val				
94	140	145	150		
96	tcg gtg gta gtg att cct ggt gat atc gct aag gaa gac gca ggt gac			833	
97	Ser Val Val Ile Pro Gly Asp Ile Ala Lys Glu Asp Ala Gly Asp				
98	155	160	165		
100	ggt act tat tcc aat tcc act att tct tct ggc act cct gtg gtg ttc			881	
101	Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr Pro Val Val Phe				
102	170	175	180	185	
104	ccg gat cct act gag gct gca gcg ctg gtg gag gcg att aac aac gct			929	
105	Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala Ile Asn Asn Ala				
106	190	195	200		
108	aag tct gtc act ttg ttc tgc ggt gcg ggc gtg aag aat gct cgc gcg			977	
109	Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys Asn Ala Arg Ala				
110	205	210	215		
112	cag gtg ttg gag ttg gcg gag aag att aac tca ccg atc ggg cat gcg			1025	
113	Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro Ile Gly His Ala				
114	220	225	230		
116	ctg ggt aag cag tac atc cag cat gag aat ccg ttt gag gtc ggc			1073	
117	Leu Gly Gly Lys Glu Tyr Ile Gln His Glu Asn Pro Phe Glu Val Gly				
118	235	240	245		
120	atg tct ggc ctg ctt ggt tac ggc gcc tgc gtg gat gcg tcc aat gag			1121	
121	Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp Ala Ser Asn Glu				
122	250	255	260	265	
124	gcg gat ctg ctg att cta ttg ggt acg gat ttc cct tat tct gat ttc			1169	
125	Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro Tyr Ser Asp Phe				
126	270	275	280		
128	ttt cct aaa gac aac gtt gcc cag gtc gat atc aac ggt gct gac att			1217	
129	Ile Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn Gly Ala His Ile				
130	285	290	295		
132	ggt cga cgt acc acg gtg aag tat ccg gtc acc ggt gat gtt gct gca			1265	
133	Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly Asp Val Ala Ala				
134	300	305	310		

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136 aca atc gaa aat att ttg cct cat gtg aag gaa aac aca gat cgt tcc	1313
137 Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys Thr Asp Arg Ser	
138 315 320 325	
140 ttc ctt gat cgg atg ctc aag gca cac gag cgt aag ttg agc tcg gtg	1361
141 Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys Leu Ser Ser Val	
142 330 335 340 345	
144 gta gag acg tac aca cat aac gtc gag aag cat gtg cct att cac cct	1409
145 Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val Pro Ile His Pro	
146 350 355 360	
148 gag tac gtt gcc tct att ttg aac gag ctg gcg gat aag gat gcg gtg	1457
149 Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp Lys Asp Ala Val	
150 365 370 375	
152 ttt act gtg gat acc ggc atg tgc aat gtg tgg cat gcg agg tac atc	1505
153 Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His Ala Arg Tyr Ile	
154 380 385 390	
156 gag aat ccg gag gga acg cgc gac ttt gtg ggt tca ttc cgc cac ggc	1553
157 Glu Asn Pro Glu Gly Thr Arg Asp Phe Val Gly Ser Phe Arg His Gly	
158 395 400 405	
160 acg atg gct aat gcg ttg cct cat gcg att ggt gcg caa agt gtt gat	1601
161 Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala Gln Ser Val Asp	
162 410 415 420 425	
164 cga aac cgc cag gtg atc gcg atg tgt ggc gat ggt ggt ttg ggc atg	1649
165 Arg Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly Gly Leu Gly Met	
166 430 435 440	
168 ctg ctg ggt gag ctt ctg acc gtt aag ctg cac caa ctt ccg ctg aag	1697
169 Leu Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln Leu Pro Leu Lys	
170 445 450 455	
172 gct gtg gtg ttt aac aac agt tct ttg ggc atg gtg aag ttg gag atg	1745
173 Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val Lys Leu Glu Met	
174 460 465 470	
176 ctc gtg gag gga cag cca gaa ttt ggt act gac cat gag gaa gtg aat	1793
177 Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His Glu Glu Val Asn	
178 475 480 485	
180 ttc gca gag att gcg gcg gct gcg ggt atc aaa tcg gta cgc atc acc	1841
181 Phe Ala Glu Ile Ala Ala Ala Gly Ile Lys Ser Val Arg Ile Thr	
182 490 495 500 505	
184 gat ccg aag aaa gtt cgc gag cag ctc gct gag gca ttg gca tat cct	1889
185 Asp Pro Lys Val Lys Val Arg Glu Gln Leu Ala Glu Ala Leu Ala Tyr Pro	
186 510 515 520	
188 gga cct gta ctg atc gat atc gtc acg gat cct aat gcg ctg tcg atc	1937
189 Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn Ala Leu Ser Ile	
190 525 530 535	
192 cca cca acc acc atc acg tgg gaa cag gtc atg gga ttc acg aag gcg gcc	1985
193 Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe Ser Lys Ala Ala	
194 540 545 550	
196 acc cga acc gtc ttt ggt gga gga gta gga gcg atg atc gat ctg gcc	2033
197 Thr Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met Ile Asp Leu Ala	
198 555 560 565	
200 cgt teg aac ata agg aat att cct act cca tggatgttga tacaccgtgt	2083

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201 Arg Ser Asn Ile Arg Asn Ile Pro Thr Pro
202 570 575
204 gttctcatgtt accgcgagctttaactgcc aacatttcca ggatggcagtcacgcgggt 2143
206 gccccatgaga ttgcct 2160
209 <210> SEQ ID NO: 2
210 <211> LENGTH: 579
211 <212> TYPE: PRT
212 <213> ORGANISM: Corynebacterium glutamicum
214 <400> SEQUENCE: 2
216 Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln
217 1 5 10 15
220 Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
221 20 25 30
224 Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
225 35 40 45
228 Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
229 50 55 60
232 Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
233 65 70 75 80
236 Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
237 85 90 95
240 Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Gln
241 100 105 110
244 Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
245 115 120 125
248 Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
249 130 135 140
252 Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly
253 145 150 155 160
256 Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
257 165 170 175
260 Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
261 180 185 190
264 Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys
265 195 200 205
268 Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
269 210 215 220
272 Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Lys Gln Tyr Ile
273 225 230 235 240
276 Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
277 245 250 255
280 Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu
281 260 265 270
284 Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
285 275 280 285
288 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
289 290 295 300
292 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
293 305 310 315 320

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\11072001\I965825.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date